Illumina TruSight™ Software Suite Release Notes

v.2.0.1

February 2021

Introduction

TruSight™ Software Suite (TSS) is designed for translating genomic sequencing data in meaningful, interpretable results in rare disease cases. Highlights include:

Comprehensive, ultra-rapid variant calling

Use DRAGEN™ secondary analysis to call small variants, structural variants, mitochondrial variants, repeat expansions, runs of homozygosity, and SMN1/SMN2 variants.

Simplified, customizable case management

Manage cases from sample acquisition to report, assign cases to users, configure pipeline settings, and set quality control (QC) thresholds.

Intuitive, high-powered interpretation and reporting

Filter variants via gene lists, inheritance modes, custom annotations, and complex logic; flag, sort, and prioritize important variants; use customizable reporting templates.

Secure, compliant environment

TruSight Software Suite has been independently audited and certified for HIPAA compliance, ISO27001, and ISO13485. It is built to enable data privacy and compliance with the principles of GDPR.

These Release Notes detail the key features and changes to software components for the release of TruSight Software Suite v.2.0.1 For information on how to use the system, see the TruSight Software Suite Online Help. TruSight Software Suite is a comprehensive solution for alignment, variant calling, variant annotation, filtering, interpretation, curation, and reporting, including features such as:

- Automatic secondary analysis with DRAGEN™ and annotation of:
  - Small Variants, CNVs, SVs, Mitochondrial variants, ROH, STRs, SMA
- Support for whole genome and whole exome sequencing
- Sequencer and BaseSpace Sequence Hub Integration
- Case Dashboard and Test Management
- IGV Visualization
- Up-to-date annotations from Nirvana and custom annotations
- Complex custom filters and gene lists from phenotypes
- SpliceAI & PrimateAI and AI-based variant prioritization via Emedgene
- Storage of variant curation
- Visualization of aggregate data for genes or variants
- Customized report generation
- Audit logging
- API documentation

Release v.2.0.1 Updates

This release includes updates to backend architecture and other performance enhancing updates. TSS is now able to support data migration between versions of the software. There are no feature updates.

MIGRATE CASES TO NEW VERSION

After a new version of the software is released, you can continue to use the older version for 90 days while evaluating the new version in a preview environment. During the 90-day preview period, Illumina can migrate a limited number of open cases to the new version. After 90 days, all accounts are automatically upgraded to the upgraded version. Unmigrated open cases are not carried over.

1. Prepare your account for migration.

Close cases that no longer require review. Limit the number of open cases to less than 50. Wait for any cases with a status of In Progress — Processing to complete. Evaluate the new version. The new version is available for 90 days at https://<yourdomain>.preview.trusight.illumina.com.

2. Contact Illumina support to schedule the migration.

Plan for approximately 24 hours of system downtime. Total downtime depends on the number of open cases.

3. After migration is complete, review open cases.

Case info, status, and substatus data are transferred, however some case statuses are changed and might require reprocessing.

Status in Old Version		Status in New Version		Action
Status	**Substatus**	**Status**	**Substatus**	
In Progress	QC Warning	In Progress	Has Issues	Reprocess the case.
In Progress	Failed to process phenotype overlap	In Progress	Has Issues	Reprocess the case.
In Progress	Failed to process pathogenicity	In Progress	Has Issues	Reprocess the case.
In Progress	Ready for Interpretation	In Progress	Ready for Interpretation	Reinterpret the case.
In Progress	Ready for Review	In Progress	Ready for Interpretation	
Complete	Reports Available	Complete	Closed	

VERSIONS

Versions of component software

- TruSight Software Suite v.2.0.1 runs multiple DRAGEN versions for secondary analysis:
    - Whole genome v.3.5.7b
    - Whole genome v.3.7.5
    - Whole exome v.3.7.5
- TSS v.2.0.1 uses Nirvana v.3.12 for annotation
- TSS v.2.0.1 uses KNS-API v.0.12.0 and KNS-UI v.0.2.0- for curation
- TSS v.2.0.1 uses CLI v.2.0.1
- TSS v.2.0.1 uses Emedgene pipeline v.03.55 / 05.00

RESOLVED ISSUES

Defect repairs (bug fixes) from v2.0.0.1 release:

- Cases with variants that have ClinVar significance "no interpretation for the single variant" will fail.
- STRs at the same position and with the same consequence do not share nucleotide and variant details associations.

KNOWN LIMITATIONS

- When running cases with non-HPO terms, Emedgene variant prioritization feature is not supported. Workaround is to run this case without Emedgene functionality with tech support.
- The joint genotyping of the parents in extended pedigrees may not be based on the probands genotype, but rather the last child specified in the pedigree file. This does not affect duos or trios, and only affects cases with 4 or 5 family members.
- After adding a case to CaseLog, alternative allele frequency is not updated in the CaseLog summary.

Open known issues from previous releases can be found in TruSight Software Suite Release Notes v.2.0.0.1 and earlier:

https://support.illumina.com/downloads/trusight-software-suite-release-notes.html